

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-695-369a-27.res made by bobryen on Mon 24 Feb 10 13:25:08 PST.

query sequence being compared: US-09-695-369A-27 (1-297)

Number of sequences searched:	6
Number of scores above cutoff:	6

Results of the initial comparison of US-09-695-369A-27 (1-297) with:
File : new.seq

	100-
N	-
T	50-
A	-
B	-
E	-
R	-
O	10-
F	-
S	5-
E	-
Q	-
U	-
V	-
E	-
N	-
C	-
S	0-
	** *
SCORE	0 1 26 52 78 104 131 157 183 209 235
STDEV	0 1 1 1 1 1 1 1 1 1 1

	*

PARAMETERS		
Similarity matrix	PAM-150	1
Threshold level of sim.	16%	
Translation Frame	6	
Match penalty	1	20
Mismatch penalty	5.00	297
G _c size penalty	0.05	
Cutoff score	1	
Randomization group	0	

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
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Times:	CPU	Total Elapsed
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Number of residues:	1857
Number of sequences searched:	6
Number of scores above cutoff:	6

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Init.	Opt.	Length	Score	Score	Sig.	Frame
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	****	2 standard deviations above mean	****	
1. US-09-840-795-18 Sequence 18, Application	310	235	237	2.04
**** 0 standard deviation from mean ****				
2. US-09-840-795-18 Sequence 18, Application	309	22	128	-0.33
3. US-09-840-795-18 Sequence 18, Application	309	17	123	-0.39
4. US-09-840-795-18 Sequence 18, Application	310	15	124	-0.41
5. US-09-840-795-18 Sequence 18, Application	309	13	112	-0.44
6. US-09-840-795-18 Sequence 18, Application	310	11	117	-0.46

1. US-09-695-369A-27 (1-297)
US-09-840-795-18 Sequence 18, Application US/09840795

Initial Score	=	235	Optimized Score	=	237	Significance	=	2.04
Residue Identity	=	72%	Matches	=	213	Mismatches	=	71
Gaps	=	8	Conservative Substitutions	=			=	1
Translation Frame	=	3						

10 60 70 80 90 100 110 120 130 140
 WGHKKQSCITCAVINRYQKVNCTATSNVACGDCLPFFYKTRIGLQDQDECIPCTKQFPTSEVQCAFQLSL
 WGHKKQSCITCAVINRYQKVNCTATSNVACGDCLPFFYKTRIGLQDQDECIPCTKQFPTSEVQCAFQLSL
 80 90 100 110 120 130 140
 WGHKKQSCITCAVINRYQKVNCTATSNVACGDCLPFFYKTRIGLQDQDECIPCTKQFPTSEVQCAFQLSL
 10 20 30 40 50 60 70
 VPESHIGARAIISSVTGLPMDCCQENELWQDQWGRVCYICQRCGPQGLSKDCGEGGDAYCTACPPRRYKSS
 10 20 30 40 50 60 70
 VPESHIGARAIISSVTGLPMDCCQENELWQDQWGRVCYICQRCGPQGLSKDCGEGGDAYCTACPPRRYKSS

130 140 150 160 170 180 190
VEADAPFVPOEATLVALVSLIVFTTIAFLIGLIFELCYKQFENRHCQRGGLIQFEADKTAKEESLFPVPSK
VEADAPFVPOEATLVALVSLIVFTTIAFLIGLIFELCYKQFENRHCQRGGLIQFEADKTAKEESLFPVPSK
VEADAPFVPOEATLVALVSLIVFTTIAFLIGLIFELCYKQFENRHCQRGGLIQFEADKTAKEESLFPVPSK
150 160 170 180 190 200 210 220

200 210 220 230 240 250 260
 ETSAESGVSENI FQTOPNPILEDSCSTSGFP TQSEFTMA SCSTESHVWHSPIE CTELDLQKRTSSASY
 ||||| || |
 ETSAESGVWAPGSLA L-----FSLDSVP I PQQQGGP EMXCFQEL I PRWGISTYPI PPDHXSSISQGL
 230 240 250 260 270 280

270	280	290	X
TGAETLTGNTVESTGDRLELNVPFEVPS			
:			
IWSISCFPVVVMGARFHIGTTRHV			
290	300	310	

2. US-09-695-369A-27 (1-297)
US-09-840-795-18 Sequence 18, Application US/09840795

Initial Score	=	22	Optimized Score	=	128	Significance	=	-0.33
Residue Identity	=	7%	Matches	=	23	Mismatches	=	258
Gaps	=	0	Conservative Substitutions	=			=	16
Translation Frame	=	4						

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X      10      20      30      40      50      60
MDCQENEMYDQWGRCVTCQRCRGPQELSDCQYGEEDAYCTACPPRRYKSSWGHHKCQSCITC
:      :      :      :      :      :
MSGSPMAYVESGSPDIYKEARNAPDQSLXNGESTLWMDGIGYAPSVGYXLVWTSHERPULLLWYRNKVRQEQ
10      20      30      40      50      60      70

70      80      90      100     110     120     130
AVINRYOKVNCIATASNAVCGDCLPRFPRKTRIGGQDQECIPCTKQPTSEVQCAFQJSLVEADAPTVPQOE
      |      :      :      :      :
LGKARGBRDGLSTGLLAGWHEBERLLCCFISLKLQQTSLAMSVELLAVEEEPQOEQGGKHHXOAAHQ
80      90      100     110     120     130     140

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[illegible]

3 -09-695-369A-27 (1-297)
US-09-840-795-18 Sequence 18, Application US/09840795

Initial Score	=	17	Optimized Score	=	123	Significance	=	-0.39
Residue Identity	=	10%	Matches	=	32	Mismatches	=	241
Gaps	=	8	Conservative Substitutions				=	15
Translation Frame	=	5						

X 10 20 30 40 50
 MDQENEYWDWGRCVTCQRCGP-----QELSKDCGYGEGSDAYCTACPPRRYKSSWG
 | | | | |
 TCLVPPXMMNLAPQTTTGKQEMLQISPCEMENQSSGSGXMDPHLXGISCGHHISGPCCCGIGTESRENNN
 10 X 20 30 40 50 60 70

	60	70	80	90	100	110	120
HMHQSCITCAVINRQKYNCTATSNAYCGDCLPRYRKTRIGLODOECIPCKQTPTSEVOCAFOLIVE		:	:	:			
WARLPGAQETWDSALVILGCTGRDSSFAYLVASNCSKPFRWCILKNCLQXKKSPKRAKVNTTSRLTSS							
	80	90	100	110	120	130	140

130 140 150 160 170 180 190
ADAPTVPQ~~EA~~IALVALVSSILIVFTLAEFLGLFYLYCKQ~~FN~~RHCQ~~RG~~L--LQFEADKTAKEESLFPVPPS
| | | | | : | | |
AFSTASXGFTGASASTKLNMKAHXTSEVGVCFVHGMSWSCRPDMRVFRXNLGKQSPQ~~FL~~EAVALVLTFTXT
150 160 170 180 190 200 210

200	210	220	230	240	250	260
KETSAESQVSENIFOTOPINPILLEDSCSTSGFPQGESFTMASCTSESHSHWASPICTELDLQKSSAS						
220	230	240	250	260	270	280
ALMTAQVMOLXLMWPOLLILYLRGQAVQXASPPSPXQSLDSCGPHRMOVYTHRPHNSQYSFSWQSNVGR						

270 280 290
YTGAEITLGNTVESTGDRLEINVPFEVPS
| :: |
PVTDEXMALAPKWDSGTNDQ
290 300 X

4. US-09-695-369A-27 (1-297)

US-09-840-795-18 Sequence 18, Application US/09840795

Initial Score	=	15	Optimized Score	=	124	Significance	=	-0.41
Residue Identity	=	10%	Matches	=	31	Mismatches	=	248
Gaps	=	9	Conservative Substitutions					10
Translation Frame	=	1						

X 10 20 30 40 50 60
MDCQENYWDWGRCTVTCQRCGPQELSKDCG-YGEGDAYCTACPRPRXRKSSWGHHKQSCITTCAVIN
| : | | : | : | :
RAEVDLYRSPTEQEPSTRPLPAFPFWIAKKMSTGTNGDVSPPANGVILDRSTPRIVMEREMPTAPALL
X 10 20 30 40 50 60 70

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70      80      90      100      110      120      130      140
RVQKVNCTATSNVAVCGDCLPRFRYRKTRIGLQDQECIPCTKQTPTSEYQCAFQLSLYEADAPTVPPQAEATIV
      |      |      |      |      |      |      |      |
      1      2      3      4      5      6      7      8
AGTKAGATTNVAVASPYLSSIVFRSTQAQLPMLSTGYVCPGSTE-----RHALLACRTKASARARSR
      80      90      100      110      120      130

ALVSSLIVFTTLAFLGLEFFLYCKQFENRHCQRGGLQFEADKTAKESLFPVPPSKETSASQSYSENIQOTQ
      150      160      170      180      190      200      210
      |      |      |      |      |      |      |
      1      2      3      4      5      6      7
PPPLRFNVSSXAXWROMHPQCPILRRPHLLHWXAACXWCLPWPSPWSSSSSTASSSTDIASVEVCCSLRLIK
      140      150      160      170      180      190      200

      220      230      240      250      260      270      280
PLNPILEDCCSSTSGFPQESTMASCTSESHSHWVSPICECTELDQKFISSASATGAFTLGGNTVESTGD
      |      |      |      |      |      |      |
      1      2      3      4      5      6      7
OQRRLNSPCHPARRPVLPKSLGPLALPSCSLWTLFLYHNSRGLKCDVHTSXPPTDGAYPIPSHORIDS
      210      220      230      240      250      260      270      280

      290      X
RLELNVPEFVPPSP
      :
PFHKDXSGAFLASLLXSGEPDSTFMGLPDM
      290      X      300      310

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5. US-09-695-369A-27 (1-297)
US-09-840-795-18 Sequence 18, Application US/09840795

Initial Score	=	13	Optimized Score	=	111	Significance	=	-0.44
Residue Identity	=	9%	Matches	=	27	Mismatches	=	242
Gaps	=	3	Conservative Substitutions					9
Translation Frame	=	6						

10 20 30 40 50 60 70
MDCQENEMYDWQHGCVTCQRCGPQGLSKDCGYGEGDAYCTACDEPRRYKSSWGHHKQCSCTCAVINRQOR
| | | | | | | | | |
HWWXSHCEGIMLPRLOQGSKKCSRSYLWKWRINPLGWDRICTPICRVLALVD
X 10 20 30 40 50

VNCTATSNVAVCGDCLPRFYRKRIGG--IQDOECIPOTKQPTSEVOCAFQSLVEADAPVPPOEATYVAL
80 90 100 110 120 130 140
: | | | | |
TFQAPAAVVVXESPERTTGGCQGCKRKRGTOHMSPPWVARGREITPLLFFQDOTAANLHAGNVWCXRTRACSRS
60 70 80 90 100 110 120

150 160 170 180 190 200 210
VSLIYVETIAFLGLFELYCKQFFNRHCGLLQFMADKTAKESLFPVPPEKETSAESQVSENI -PQLQP
| : | : | : | : | :
GRAPGRPGXTPLAGCSPVOQVWPPREGALMVHLPLPLSTGRHIEQRMGSASCTGCTLLGPAGLQCVSFGRTW
130 140 150 160 170 180 190

220	230	240	250	260	270	280
LNPILEDDCSSSTGCFPTQESPTMASCTSSSHSHWVHSP						
	1			1	1	1
1						
ANSPHRQHXRLXCSXPS	EHDXQHRXCNSD	ICGGPSCFCTCE	EGRLCSRHLPL	HNHNPNWIA	PVQDHTVGRX	
200	210	220	230	240	250	260

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290      X
      LELNPFEEVPS
      :
HTVP:IGPSTHFLGNPWEGRXRTSRNLLPNG
270      280      290      300

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6. US-09-695-369A-27 (1-297)

US-09-840-795-18 Sequence 18, Application US/09840795

Initial Score	=	11	Optimized Score	=	117	Significance	=	-0.46
Residue Identity	=	7%	Matches	=	24	Mismatches	=	261
Gaps	=	12	Conservative Substitutions				=	12
Translation Frame=		2						

X	10	20	30	40	50	60
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MDCQENEYWDQWGRVCVTCQRCGPGQGLSLDCCGYEGEGGAYCTACP---PRRYKSSWGHHKQCOSCITCAVIN
:
ALRWICTGVPIRGSKSHLLVRYRPSHHGLPRKXVLGPMGTVCHLPTVMSWTGAIQGLWLMRGWRCLLSLPSS
X 10 20 30 40 50 60 70
70 80 90 100 110 120 130 140
RVQKVNCTAITSNAVCGDCLPRFYRKTRIGLQDQECIPCTKQTPITSEYQCAFQLSLYEADAPITVPPQEA TLV
||| |
QVQKQLGPPQMSLHHLCCQHOSCSEGQLSHYLXCCLMGTFQAQVLPKDTHWRPAGPRVHPVHEADPHLXGSMC
80 90 100 110 120 130 140
150 160 170 180 190 200
ALVSSLVAVFLLAFLGLFLYCKQ-----FENRHQCRGGLLOFEADKTAKESLSEVPPSKESLSAESQVS
| : |
LPVELSGGRCHTSAPSGGHTTCCTGEQBPASGVYRGLPQALLPILQAVLQOTLPAMRPAAYXGXNKGISLP
150 160 170 180 190 200 210
210 220 230 240 250 260 270
ENIFOTQF--LNPILLEDCCSSTSGFPTQESFTMASCFESHSHWVHSPIECTELDLQKFSSASAYTGAEFTIG
| | : : :
RATQGDQDCXVPSILGPMQPCPVVLSGLCSYTTTAAAGAXNMVSTRANTLQMGHILSHPTRGLLHFTRTDLE
220 230 240 250 260 270 280
280 290 X
GNTVESTGDRLELNVPEEVPSP
:
HFLLPCCSLGSOIPHSWDYQTC
290 300 310

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